OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/804,626

DATE: 03/30/2001
TIME: 15:02:53

Input Set : A:\PTO.txt
Output Set: N:\CRF3\03302001\I804626.raw

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       3 <110> APPLICANT: Lobel, Leslie
       4        Lustbader, Joyce
       6 <120> TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR
DOMAIN OF A
       7        GONADOTROPIN RECEPTOR
       9 <130> FILE REFERENCE: 0575/62259/JPW/SHS
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/804,626
C--> 11 <141> CURRENT FILING DATE: 2001-03-09
      11 <160> NUMBER OF SEQ ID NOS: 8
      13 <170> SOFTWARE: PatentIn version 3.0
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      16 <211> LENGTH: 1557
      17 <212> TYPE: DNA
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      25 ccgattctgg atgaaatcgc tgacgaatat cagggcaaac tgaccgttgc aaaactgaac     180
      27 atcgatcaaa accctggcac tgcgccgaaa tatggcatcc gtggtatccc gactctgctg     240
      29 ctgttcaaaa acggtgaagt ggcggcaacc aaagtgggtg cactgtctaa aggtcagttg     300
      31 aaagagttcc tcgacgctaa cctggccggt tctggttctg ccatatgca ccatcatcat     360
      33 catcattctt ctggtctggt gccacgcggt tctggtatga agaaaccgc tgctgctaaa     420
      35 ttcgaacgcc agcacatgga cagcccagat ctgggtaccg acgacgacga caaggccatg     480
      37 gctgatatcg gatccgaatt ccgagcgctg cgcgaggcgc tctgccctga ccctgcaac     540
      39 tgcgtgcccg acggcgccct gcgctgcccc ggccccacgg ccggtctcac tcgactatca     600
      41 cttgcctacc tccctgtcaa agtgatccca tctcaagctt tcagaggact taatgaggtc     660
      43 ataaaaattg aaatctctca gattgattcc ctggaaagga tagaagctaa tgcctttgac     720
      45 aacctcctca atttgtctga aatactgatc cagaacacca aaaatctgag atacattgag     780
      47 cccggagcat ttataaatct tccccgatta aaatacttga gcatctgtaa cacaggcatc     840
      49 agaaagtttc cagatgttac gaaggtcttc tcctctgaat caaatttcat tctggaaatt     900
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      53 tctgtaacac tcaaactata tggaaatgga tttgaagaag tacaaagtca tgcattcaat    1020
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      67 ctttattctt ccatgcttgc tgagagtgaa ctgagtggct gggactatga atatggtttc    1440
      69 tgcttaccca agacaccccg atgtgctcct gaaccagatg ctttaatcc ctgtgaagat    1500
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3/30/01

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 87 Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
 88          35              40              45
 90 Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn
 91     50              55              60
 93 Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
 94 65                  70              75                  80
 96 Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
 97                  85              90                  95
 99 Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
100              100             105             110
102 Ser Gly His Met His His His His His His Ser Ser Gly Leu Val Pro
103          115             120             125
105 Arg Gly Ser Gly Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln
106     130             135             140
108 His Met Asp Ser Pro Asp Leu Gly Thr Asp Asp Asp Asp Lys Ala Met
109 145             150             155             160
111 Ala Asp Ile Gly Ser Glu Phe Arg Ala Leu Arg Glu Ala Leu Cys Pro
112              165             170             175
114 Glu Pro Cys Asn Cys Val Pro Asp Gly Ala Leu Arg Cys Pro Gly Pro
115              180             185             190
117 Thr Ala Gly Leu Thr Arg Leu Ser Leu Ala Tyr Leu Pro Val Lys Val
118          195             200             205
120 Ile Pro Ser Gln Ala Phe Arg Gly Leu Asn Glu Val Ile Lys Ile Glu
121     210             215             220
123 Ile Ser Gln Ile Asp Ser Leu Glu Arg Ile Glu Ala Asn Ala Phe Asp
124 225             230             235             240
126 Asn Leu Leu Asn Leu Ser Glu Ile Leu Ile Gln Asn Thr Lys Asn Leu
127              245             250             255
129 Arg Tyr Ile Glu Pro Gly Ala Phe Ile Asn Leu Pro Arg Leu Lys Tyr
130          260             265             270
132 Leu Ser Ile Cys Asn Thr Gly Ile Arg Lys Phe Pro Asp Val Thr Lys
133          275             280             285
135 Val Phe Ser Ser Glu Ser Asn Phe Ile Leu Glu Ile Cys Asp Asn Leu
136     290             295             300
138 His Ile Thr Thr Ile Pro Gly Asn Ala Phe Gln Gly Met Asn Asn Glu
139 305             310             315             320
141 Ser Val Thr Leu Lys Leu Tyr Gly Asn Gly Phe Glu Glu Val Gln Ser
142          325             330             335
144 His Ala Phe Asn Gly Thr Thr Leu Thr Ser Leu Glu Leu Lys Glu Asn
145          340             345             350
147 Val His Leu Glu Lys Met His Asn Gly Ala Phe Arg Gly Ala Thr Gly
148          355             360             365
150 Pro Lys Thr Leu Asp Ile Ser Ser Thr Lys Leu Gln Ala Leu Pro Ser
151     370             375             380
153 Tyr Gly Leu Glu Ser Ile Gln Arg Leu Ile Ala Thr Ser Ser Tyr Ser
154 385             390             395             400
156 Leu Lys Lys Leu Pro Ser Arg Glu Thr Phe Val Asn Leu Leu Glu Ala
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Input Set : A:\PTO.txt
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159 Thr Leu Thr Tyr Pro Ser His Cys Cys Ala Phe Arg Asn Leu Pro Thr
160             420                 425                 430
162 Lys Glu Gln Asn Phe Ser His Ser Ile Ser Glu Asn Phe Ser Lys Gln
163         435                 440                 445
165 Cys Glu Ser Thr Val Arg Lys Val Asn Asn Lys Thr Leu Tyr Ser Ser
166     450                 455                 460
168 Met Leu Ala Glu Ser Glu Leu Ser Gly Trp Asp Tyr Glu Tyr Gly Phe
169 465                 470                 475                 480
171 Cys Leu Pro Lys Thr Pro Arg Cys Ala Pro Glu Pro Asp Ala Phe Asn
172             485                 490                 495
174 Pro Cys Glu Asp Ile Met Gly Val Asp Lys Leu Ala Ala Ala Leu Glu
175         500                 505                 510
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181 <211> LENGTH: 1551
182 <212> TYPE: DNA
183 <213> ORGANISM: Homo Sapiens
185 <400> SEQUENCE: 3
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188 gacggggcga tcctcgtcga tttctgggca gagtggtgcg gtccgtgcaa aatgatcgcc   120
190 ccgattctgg atgaaatcgc tgacgaatat caggggcaaac tgaccgttgc aaaaactgaac  180
192 atcgatcaaa accctggcac tgcgccgaaa tatggcatcc gtggtatccc gactctgctg   240
194 ctgttcaaaa acggtgaagt ggcggcaacc aaagtgggtg cactgtctaa aggtcagttg   300
196 aaagagttcc tcgacgctaa cctggccggt tctggttctg gccatatgca ccatcatcat   360
198 catcattctt ctggtctggt gccacgcggt tctggtatga agaaaccgc tgctgctaaa    420
200 ttcgaacgcc agcacatgga cagcccagat ctgggtaccg acgacgacga caaggccatg   480
202 gctgatatcg gatccgaatt caggggttttt ctctgccaag agagcaaggt gacagagatt   540
204 ccttctgacc tcccgaggaa tgccattgaa ctgaggtttg tcctcaccaa gcttcgagtc   600
206 atccaaaaag gtgcattttc aggatttggg gacctggaga aaatagagat ctctcagaat   660
208 gatgtcttgg aggtgataga ggcagatgtg ttctccaacc ttcccaaatt acatgaaatt   720
210 agaattgaaa aggccaacaa cctgctctac atcacccctg aggccttcca gaaccttccc   780
212 aaccttcaat atctgttaat atccaacaca ggtattaagc accttccaga tgttcacaag   840
214 attcattctc tccaaaaggt tttacttgac attcaagata acataaacat ccacacaatt   900
216 gaaagaaatt ctttcgtggg gctgagcttt gaaagtgtga ttctatggct gaataagaat   960
218 gggattcaag aaatacacaa ctgtgcattc aatggaaccc aactagatgc agtgaatcta  1020
220 agcgataata ataatttaga agaattgcct aatgatgttt ccacggagc ctctggacca   1080
222 gtcattctag atatttcaag aacaaggatc cattccctgc ctagctatgg cttagaaaat  1140
224 cttaagaagc tgagggccag gtcgacttac aacttaaaaa agctgcctac tctggaaaag  1200
226 cttgtcgccc tcatggaagc cagcctcacc tatcccagcc attgctgtgc ctttgcaaac  1260
228 tggagacggc aaatctctga gcttcatcca atttgcaaca aatctatttt aaggcaagaa  1320
230 gttgattata tgactcaggc taggggtcag agatcctctc tggcagaaga caatgagtcc  1380
232 agctacagca gaggatttga catgacgtac actgagtttg actatgactt atgcaatgaa  1440
234 gtggttgacg tgacctgctc ccctaagcca gatgcattca acccatgtga agatatcatg  1500
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239 <210> SEQ ID NO: 4
240 <211> LENGTH: 516
241 <212> TYPE: PRT
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242 <213> ORGANISM: Homo Sapiens
244 <400> SEQUENCE: 4
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250   20   25   30
252 Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
253   35   40   45
255 Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn
256   50   55   60
258 Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
259 65   70   75   80
261 Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
262   85   90   95
264 Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
265   100   105   110
267 Ser Gly His Met His His His His His His Ser Ser Gly Leu Val Pro
268   115   120   125
270 Arg Gly Ser Gly Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln
271   130   135   140
273 His Met Asp Ser Pro Asp Leu Gly Thr Asp Asp Asp Asp Lys Ala Met
274 145   150   155   160
276 Ala Asp Ile Gly Ser Glu Phe Arg Val Phe Leu Cys Gln Glu Ser Lys
277   165   170   175
279 Val Thr Glu Ile Pro Ser Asp Leu Pro Arg Asn Ala Ile Glu Leu Arg
280   180   185   190
282 Phe Val Leu Thr Lys Leu Arg Val Ile Gln Lys Gly Ala Phe Ser Gly
283   195   200   205
285 Phe Gly Asp Leu Glu Lys Ile Glu Ile Ser Gln Asn Asp Val Leu Glu
286   210   215   220
288 Val Ile Glu Ala Asp Val Phe Ser Asn Leu Pro Lys Leu His Glu Ile
289 225   230   235   240
291 Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Thr Pro Glu Ala Phe
292   245   250   255
294 Gln Asn Leu Pro Asn Leu Gln Tyr Leu Leu Ile Ser Asn Thr Gly Ile
295   260   265   270
297 Lys His Leu Pro Asp Val His Lys Ile His Ser Leu Gln Lys Val Leu
298   275   280   285
300 Leu Asp Ile Gln Asp Asn Ile Asn Ile His Thr Ile Glu Arg Asn Ser
301   290   295   300
303 Phe Val Gly Leu Ser Phe Glu Ser Val Ile Leu Trp Leu Asn Lys Asn
304 305   310   315   320
306 Gly Ile Gln Glu Ile His Asn Cys Ala Phe Asn Gly Thr Gln Leu Asp
307   325   330   335
309 Ala Val Asn Leu Ser Asp Asn Asn Leu Glu Glu Leu Pro Asn Asp
310   340   345   350
312 Val Phe His Gly Ala Ser Gly Pro Val Ile Leu Asp Ile Ser Arg Thr
313   355   360   365
315 Arg Ile His Ser Leu Pro Ser Tyr Gly Leu Glu Asn Leu Lys Lys Leu

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316     370                     375                 380
318 Arg Ala Arg Ser Thr Tyr Asn Leu Lys Lys Leu Pro Thr Leu Glu Lys
319 385                     390                 395                 400
321 Leu Val Ala Leu Met Glu Ala Ser Leu Thr Tyr Pro Ser His Cys Cys
322                 405                 410                 415
324 Ala Phe Ala Asn Trp Arg Arg Gln Ile Ser Glu Leu His Pro Ile Cys
325                 420                 425                 430
327 Asn Lys Ser Ile Leu Arg Gln Glu Val Asp Tyr Met Thr Gln Ala Arg
328         435                 440                 445
330 Gly Gln Arg Ser Ser Leu Ala Glu Asp Asn Glu Ser Ser Tyr Ser Arg
331     450                 455                 460
333 Gly Phe Asp Met Thr Tyr Thr Glu Phe Asp Tyr Asp Leu Cys Asn Glu
334 465                 470                 475                 480
336 Val Val Asp Val Thr Cys Ser Pro Lys Pro Asp Ala Phe Asn Pro Cys
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346 <211> LENGTH: 2100
347 <212> TYPE: DNA
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397 actctagaaa gatggcacac catcacctat gctattcacc tggaccaaaa gctgcgatta   1440
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date